

## WHAT IS CLAIMED IS:

1. An isolated or recombinant polypeptide:
  - A) that:
    - 5 a) specifically binds polyclonal antibodies generated against a 12 consecutive amino acid segment of SEQ ID NO: 2; and
    - b) comprises at least one sequence selected from the following group (see SEQ ID NO: 2):
      - 10 LeuCysPheArgMetLysAsp; ValLeuTyrLeuHisAsn;  
GlnLeuLeuAlaGly; IleSerValValProAsn;  
SerProValIleLeuGlyVal; GlnCysLeuSerCysGlyThr;  
ProIleLeuLysLeuGlu; PheTyrArgArgAspMetGly;  
LeuThrSerSerPheGluSer; PheLeuCysThrSer;  
15 GlnProValArgLeuThr; PheTyrPheGlnGln;  
ArgAlaLeuAspAlaSerLeu; and GlyLeuHisAlaGluLysVal;
  - B) that:
    - 20 a) specifically binds polyclonal antibodies generated against a 12 consecutive amino acid segment of SEQ ID NO: 6; and
    - b) comprises at least one sequence selected from the following group (see SEQ ID NO: 6):
      - 25 SerLeuArgHisValGlnAsp; ValTrpIleLeuGlnAsn;  
IleLeuThrAlaVal; IleThrLeuLeuProCys;  
AspProThrTyrMetGlyVal; SerCysLeuPheCysThrLys;  
ProValLeuGlnLeuGly; PheTyrHisLysLysSerGly;  
ThrThrSerThrPheGluSer; PheIleAlaValCys;  
CysProLeuIleLeuThr; PheGluMetIleVal;  
GlnAspLeuSer; ValProArgLysGluGlnThrVal;  
30 SerLysGlySerCysPro; ArgAlaAlaSer;  
ProCysGlnTyrLeuAspThrLeuGlu; and SerGlyThrThr; or
  - C) that:
    - 35 a) specifically binds polyclonal antibodies generated against a 12 consecutive amino acid segment of SEQ ID NO: 13 or 15; and
    - b) comprises at least one sequence selected from the following group (see SEQ ID NO: 13 or 15):

ITGTIND; VWTLQG; NLVAV; VAVITC; DPIYLG I; MCLYCEK;  
PTLQLK; FYRAKTG; RTSTLES; FIASS; QPIILT; FELNI;  
SMCK; NDLN; VPR(R/S)TSVT; VPRSDSVT; TCKYPEALE;  
TGRT; SKRDQP; or SKGDQP.

5

## 2. The polypeptide of Claim 1:

- a) wherein said polypeptide comprises a plurality of  
said sequences selected from said group in  
section b) of part 1A;
- 10 b) wherein said polypeptide comprises a plurality of  
said sequences selected from said group in  
section b) of part 1B;
- c) wherein said polypeptide comprises a plurality of  
said sequences selected from said group in  
15 section b) of part 1C; or
- d) which specifically binds to polyclonal antibodies  
generated against an immunogen selected from the  
group consisting of:
- i) the polypeptide of SEQ ID NO: 2;
- 20 ii) the polypeptide of SEQ ID NO: 6;
- iii) the polypeptide of SEQ ID NO: 13; and.
- iv) the polypeptide of SEQ ID NO: 15.

## 3. The polypeptide of:

- 25 A) Claim 1A, wherein said 12 consecutive amino acid  
segment is selected from (see SEQ ID NO: 2):  
LeuCysPheArgMetLysAspSerAlaLeuLysValLeuTyrLeuHisAsn-  
Asn;  
IleSerValValProAsnArgAlaLeuAspAlaSerLeuSerProValIle-  
30 LeuGlyValGln;  
SerProValIleLeuGlyValGlnGlyGlySerGlnCys;  
ProIleLeuLysLeuGluProValAsnIleMetGluLeu;  
ThrSerSerPheGluSerAlaAlaTyrProGlyTrpPhe;  
PheLeuCysThrSerProGluAlaAspGlnProVal;  
35 ThrGlnIleProGluAspProAlaTrpAspAlaProIle; or  
ThrSerSerPheGluSerAlaAlaTyrProGlyTrpPhe;

- B) Claim 1B, wherein said 12 consecutive amino acid segment is selected from (see SEQ ID NO: 6):  
ArgAlaAlaSerProSerLeuArgHisValGlnAspLeu;  
SerSerArgValTrpIleLeuGlnAsnAsnIleLeu;  
5 ProValThrIleThrLeuLeuProCysGlnTyrLeu;  
GlyValGlnArgProMetSerCysLeuPheCysThr;  
PheCysThrLysAspGlyGluGlnProValLeuGlnLeu;  
ThrSerThrPheGluSerAlaAlaPheProGlyTrpPhe; and  
CysSerLysGlySerCysProLeuIleLeuThrGln; or
- 10 C) claim 1C, wherein said 12 consecutive amino acid segment is selected from (see SEQ ID NO: 13 or 15):  
SMCKPITGTINDL;  
NQQVWTLQGQNL;  
PVTVAVITCKYP;  
15 GIONPEMCLYCE;  
YCEKVGEQPTLQL;  
TSTLESVAFPDWF;  
SKGDQPIILTSE;  
SKRDQPIILTSE; and  
20 GKSyntAFELNIND.

3. The polypeptide of Claim 2, wherein said polypeptide:

- 25 i) is a mature protein;  
ii) lacks a post-translational modification;  
iii) is from a rodent, including a mouse;  
iv) is from a primate, including a human;  
v) is a natural allelic variant of IL-1 $\delta$  or IL-1 $\epsilon$ ;  
vi) has a length at least 30 amino acids;  
30 vii) exhibits at least two non-overlapping epitopes that are specific for a rodent IL-1 $\delta$ ;  
viii) exhibits a sequence identity over a length of at least about 20 amino acids to SEQ ID NO: 2;  
ix) exhibits at least two non-overlapping epitopes  
35 which are specific for a rodent or primate IL-1 $\epsilon$ ;  
x) exhibits a sequence identity over a length of at least about 20 amino acids to SEQ ID NO: 6 or 15;

- xi) is glycosylated;  
xii) has a molecular weight of at least 10 kD with  
natural glycosylation;  
xiii) is a synthetic polypeptide;  
5 xiv) is attached to a solid substrate;  
xv) is conjugated to another chemical moiety;  
xvi) is a 5-fold or less substitution from natural  
sequence; or  
xvii) is a deletion or insertion variant from a  
10 natural sequence.
4. A soluble polypeptide comprising:  
a) a sterile polypeptide of Claim 2;  
b) said sterile polypeptide of Claim 2 and a carrier,  
15 wherein said carrier is:  
i) an aqueous compound, including water, saline,  
and/or buffer; and/or  
ii) formulated for oral, rectal, nasal, topical,  
or parenteral administration.  
20
5. A fusion protein having a polypeptide sequence of  
Claim 2 and further comprising:  
a) a mature protein of Claim 2;  
b) a detection or purification tag, including a FLAG,  
25 His6, or Ig sequence; or  
c) sequence of another cytokine or chemokine.
6. A kit comprising a polypeptide of Claim 2, and:  
a) a compartment comprising said protein or  
30 polypeptide; and/or  
b) instructions for use or disposal of reagents in  
said kit.
7. A binding compound comprising an antigen binding  
35 site from an antibody, which specifically binds to a mature  
polypeptide from:  
a) SEQ ID NO: 2;

- b) SEQ ID NO: 6;
- c) SEQ ID NO: 13; or
- d) SEQ ID NO: 15.

5     8.           The binding compound of Claim 7, wherein:

- a) said binding compound is an Fv, Fab, or Fab2 fragment;
- b) said binding compound is conjugated to another chemical moiety; or
- 10    c) said antibody:
  - i) is raised against a polypeptide comprising a 12 consecutive amino acid segment of SEQ ID NO: 2, 6, 13, or 15;
  - ii) is raised against a mature IL-1 $\epsilon$ ;
  - 15    iii) is raised to a purified rodent IL-1 $\delta$  or rodent or primate IL-1 $\epsilon$ ;
  - iv) is immunoselected;
  - v) is a polyclonal antibody;
  - vi) binds to a denatured IL-1 $\delta$  or IL-1 $\epsilon$ ;
  - 20    vii) exhibits a K<sub>d</sub> to antigen of at least 30  $\mu$ M;
  - viii) is attached to a solid substrate, including a bead or plastic membrane;
  - ix) is in a sterile composition; or
  - x) is detectably labeled, including a
  - 25       radioactive or fluorescent label.

9.           A kit comprising said binding compound of Claim 7, and:

- a) a compartment comprising said binding compound; and/or
- 30    b) instructions for use or disposal of reagents in said kit.

10.          A composition comprising:

- 35    a) a sterile binding compound of Claim 7, or
- b) said binding compound of Claim 7 and a carrier, wherein said carrier is:

- i) an aqueous compound, including water, saline, and/or buffer; and/or
- ii) formulated for oral, rectal, nasal, topical, or parenteral administration.

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11. An isolated or recombinant nucleic acid encoding a polypeptide of Claim 2, wherein:

- a) said polypeptide of Claim 2 is IL-1 $\delta$  or IL-1 $\epsilon$  from a mammal; or
- 10 b) said nucleic acid:
  - i) comprises the mature coding sequence of SEQ ID NO: 1, 3, 12, or 14;
  - ii) encodes an antigenic peptide sequence of SEQ ID NO: 2, or SEQ ID NO: 6, 13, or 15;
  - 15 iii) encodes a plurality of antigenic peptide sequences of SEQ ID NO: 2, or SEQ ID NO: 6, 13, or 15;
  - iv) exhibits identity to a natural cDNA encoding said segment;
  - 20 v) is an expression vector;
  - vi) further comprises an origin of replication;
  - vii) is from a natural source;
  - viii) comprises a detectable label;
  - ix) comprises synthetic nucleotide sequence;
  - 25 x) is less than 6 kb, preferably less than 3 kb;
  - xi) is from a rodent or primate;
  - xii) comprises a natural full length coding sequence;
  - xiii) is a hybridization probe for a gene
  - 30 encoding said IL-1 $\delta$  or IL-1 $\epsilon$ ;
  - xiv) is a PCR primer, PCR product, or mutagenesis primer; or
  - xv) encodes an IL-1 $\delta$  or an IL-1 $\epsilon$  protein.

35 12. A cell, transformed with said nucleic acid of Claim 10.

13. The cell of Claim 12, wherein said cell is:
- a) a prokaryotic cell;
  - b) a eukaryotic cell;
  - c) a bacterial cell;
  - 5 d) a yeast cell;
  - e) an insect cell;
  - f) a mammalian cell;
  - g) a murine cell;
  - h) a primate cell; or
  - 10 i) a human cell.
14. A kit comprising said nucleic acid of Claim 11, and:
- a) a compartment comprising said nucleic acid;
  - 15 b) a compartment further comprising a mammalian IL-1 $\delta$  or IL-1 $\epsilon$  protein or polypeptide; and/or
  - c) instructions for use or disposal of reagents in said kit.
- 20 15. An isolated or recombinant nucleic acid that
- a) hybridizes under wash conditions of 40° C and less than 1M salt to SEQ ID NO: 1;
  - b) hybridizes under wash conditions of 40° C and less than 1 M salt to SEQ ID NO: 3, 5, 12 or 14.
- 25 16. The nucleic acid of Claim 15, wherein:
- a) said wash condition is at 50° C and/or 500 mM salt; and
  - b) exhibits identity over at least 20 nucleotides to
  - 30 SEQ ID NO: 1, 3, 5, 12, or 14.
17. The nucleic acid of Claim 16, wherein:
- a) a wash condition is at 65° C and/or 150 mM salt; or
  - 35 b) exhibits identity over at least 50 nucleotides to SEQ ID NO: 1, 3, 5, 12, or 14.

18. A method of modulating a cell involved in an inflammatory response comprising contacting said cell with an agonist or antagonist of a mammalian IL-1 $\delta$  or IL-1 $\epsilon$  polypeptide of Claims 1.

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19. The method of Claim 18, wherein:

- a) said contacting is in combination with an agonist or antagonist of IL-1 $\alpha$ , IL-1RA, IL-1 $\beta$ , IL-1 $\gamma$ , IL-2, and/or IL-12;
- 10 b) said contacting is with an antagonist, including binding composition comprising an antibody binding site which specifically binds an IL-1 $\delta$  or IL-1 $\epsilon$ ; or
- c) said modulating is regulation of IFN- $\gamma$  production.

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20. A method of:

- A) making an antiserum comprising an antibody of Claim 7, comprising immunizing a mammal with an immunogenic amount of:
  - 20 a) a rodent IL-1 $\delta$  polypeptide;
  - b) a peptide sequence comprising a 12 consecutive amino acid segment of SEQ ID NO: 2;
  - c) a rodent or primate IL-1 $\epsilon$  polypeptide; or
  - 25 d) a peptide sequence comprising a 12 consecutive amino acid segment of SEQ ID NO: 6, 13, or 15;thereby causing said antiserum to be produced; or
- B) producing an antigen:antibody complex, comprising
  - 30 contacting:
    - a) a rodent IL-1 $\delta$  protein or peptide with an antibody of Claim 7; or
    - b) a rodent or primate IL-1 $\epsilon$  protein or peptide with an antibody of Claim 7;
  - 35 thereby allowing said complex to form.



## SEQUENCE SUBMISSION

SEQ ID NO: 1 provides rodent IL-1 $\delta$  nucleotide sequence.  
SEQ ID NO: 2 provides rodent IL-1 $\delta$  polypeptide sequence.  
5 SEQ ID NO: 3 provides partial rodent IL-1 $\epsilon$  nucleotide sequence.  
SEQ ID NO: 4 provides partial rodent IL-1 $\epsilon$  polypeptide sequence.  
SEQ ID NO: 5 provides full length rodent IL-1 $\epsilon$  nucleic acid sequence.  
SEQ ID NO: 6 provides full length rodent IL-1 $\epsilon$  polypeptide sequence.  
SEQ ID NO: 7 provides human IL-1RA precursor polypeptide sequence.  
10 SEQ ID NO: 8 provides human IL-1 $\gamma$  (IGIF) precursor polypeptide sequence.  
SEQ ID NO: 9 provides mouse IL-1 $\gamma$  (IGIF) precursor polypeptide sequence.  
SEQ ID NO: 10 provides human IL-1 $\alpha$  precursor polypeptide sequence.  
SEQ ID NO: 11 provides human IL-1 $\alpha$  precursor polypeptide sequence.  
SEQ ID NO: 12 provides primate IL-1 $\epsilon$  nucleotide sequence.  
15 SEQ ID NO: 13 provides primate IL-1 $\epsilon$  polypeptide sequence.  
SEQ ID NO: 14 provides full length primate IL-1 $\epsilon$  nucleic acid sequence.  
SEQ ID NO: 15 provides full length primate IL-1 $\epsilon$  polypeptide sequence.

## 20 (1) GENERAL INFORMATION:

(i) APPLICANT: Hedrick, Joseph A.  
Sana, Theodore R.  
Bazan, Fernando J.  
25 Kastelein, Robert A.

(ii) TITLE OF INVENTION: Mammalian Cytokines; Related Reagents  
and Methods

30 (iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: DNAX Research Institute  
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35 (C) CITY: Palo Alto  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94304-1104

40 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

45 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE: 07-AUG-1998  
(C) CLASSIFICATION:

50 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/044,165  
(B) FILING DATE: 21-APR-1997

55 (vii) PRIOR APPLICATION DATA:  
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60 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/062,866

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## (vii) PRIOR APPLICATION DATA:

5 (A) APPLICATION NUMBER: US 09/097,976  
(B) FILING DATE: 16-JUN-1998

## (viii) ATTORNEY/AGENT INFORMATION:

10 (A) NAME: Ching, Edwin P.  
(B) REGISTRATION NUMBER: 34,090  
(C) REFERENCE/DOCKET NUMBER: DX0725K2

## (ix) TELECOMMUNICATION INFORMATION:

15 (A) TELEPHONE: 650-852-9196  
(B) TELEFAX: 650-496-1200

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 470 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

30 (A) NAME/KEY: CDS  
(B) LOCATION: 1..468

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35 ATG ATG GTT CTG AGT GGG GCA CTA TGC TTC CGA ATG AAG GAT TCA GCC 48  
Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala  
1 5 10 15

40 TTG AAG GTA CTG TAT CTG CAC AAT AAC CAG CTG CTG GCT GGA GGA CTG 96  
Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu  
20 25 30

45 CAC GCA GAG AAG GTC ATT AAA GGT GAG GAG ATC AGT GTT GTC CCA AAT 144  
His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn  
35 40 45

50 CGG GCA CTG GAT GCC AGT CTG TCC CCT GTC ATC CTG GGC GTT CAA GGA 192  
Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly  
50 55 60

55 GGA AGC CAG TGC CTA TCT TGT GGG ACA GAG AAA GGG CCA ATT CTG AAA 240  
Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys  
65 70 75 80

55 CTT GAG CCA GTG AAC ATC ATG GAG CTC TAC CTC GGG GCC AAG GAA TCA 288  
Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser  
85 90 95

60 AAG AGC TTC ACC TTC TAC CGG CGG GAT ATG GGT CTT ACC TCC AGC TTC 336  
Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe

	100	105	110	
5	GAA TCC GCT GCC TAC CCA GGC TGG TTC CTC TGC ACC TCA CCG GAA GCT Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala 115 120 125			384
10	GAC CAG CCT GTC AGG CTC ACT CAG ATC CCT GAG GAC CCC GCC TGG GAT Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp 130 135 140			432
15	GCT CCC ATC ACA GAC TTC TAC TTT CAG CAG TGT GAC TA Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp 145 150 155			470

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

1	Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala	5	10	15
20	Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu	25	30	
35	His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn	40	45	
50	Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly	55	60	
65	Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys	70	75	80
85	Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser	90	95	
100	Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe	105	110	
115	Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala	120	125	
130	Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp	135	140	
145	Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp	150	155	

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 10 (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 TTC CAG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA 48  
 Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val  
 1 5 10 15  
 20 AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT 96  
 Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe  
 20 25 30  
 25 GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG 144  
 Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly  
 35 40 45  
 30 AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT 192  
 Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr  
 50 55 60  
 35 GAC TTC GAG ATG ATT GTG GTA CAT TAA 219  
 Asp Phe Glu Met Ile Val Val His  
 65 70

35 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids  
 40 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val  
 1 5 10 15  
 50 Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe  
 20 25 30  
 Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly  
 35 40 45  
 55 Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr  
 50 55 60  
 60 Asp Phe Glu Met Ile Val Val His  
 65 70

20	GAATTCGGCA	CGAGTGTAGT	GTGCAGACAC	ATTCCCTTATT	CAATCAGGGT	CAATCTGCAG	60										
	ATTGGCAGCT	CAGGAACAAC	ATCACCATA	ATG	AAT	AAG	GAG	AAA	GAA	CTA	AGA	113					
				Met	Asn	Lys	Glu	Lys	Glu	Leu	Arg						
				1				5									
25	GCA	GCA	TCA	CCT	TCG	CTT	AGA	CAT	GTT	CAG	GAT	CTT	AGT	AGT	CGT	GTG	161
	Ala	Ala	Ser	Pro	Ser	Leu	Arg	His	Val	Gln	Asp	Leu	Ser	Ser	Arg	Val	
	10						15					20					
30	TGG	ATC	CTG	CAG	AAC	AAT	ATC	CTC	ACT	GCA	GTC	CCA	AGG	AAA	GAG	CAA	209
	Trp	Ile	Leu	Gln	Asn	Asn	Ile	Leu	Thr	Ala	Val	Pro	Arg	Lys	Glu	Gln	
	25				30						35					40	
35	ACA	GTT	CCA	GTC	ACT	ATT	ACC	TTG	CTC	CCA	TGC	CAA	TAT	CTG	GAC	ACT	257
	Thr	Val	Pro	Val	Thr	Ile	Thr	Leu	Leu	Pro	Cys	Gln	Tyr	Leu	Asp	Thr	
					45					50					55		
40	CTT	GAG	ACG	AAC	AGG	GGG	GAT	CCC	ACG	TAC	ATG	GGA	GTG	CAA	AGG	CCG	305
	Leu	Glu	Thr	Asn	Arg	Gly	Asp	Pro	Thr	Tyr	Met	Gly	Val	Gln	Arg	Pro	
				60					65					70			
45	ATG	AGC	TGC	CTG	TTC	TGC	ACA	AAG	GAT	GGG	GAG	CAG	CCT	GTG	CTA	CAG	353
	Met	Ser	Cys	Leu	Phe	Cys	Thr	Lys	Asp	Gly	Glu	Gln	Pro	Val	Leu	Gln	
			75					80					85				
50	CTT	GGG	GAA	GGG	AAC	ATA	ATG	GAA	ATG	TAC	AAC	AAA	AAG	GAA	CCT	GTA	401
	Leu	Gly	Glu	Gly	Asn	Ile	Met	Glu	Met	Tyr	Asn	Lys	Lys	Glu	Pro	Val	
	90						95					100					
55	AAA	GCC	TCT	CTC	TTC	TAT	CAC	AAG	AAG	AGT	GGT	ACA	ACC	TCT	ACA	TTT	449
	Lys	Ala	Ser	Leu	Phe	Tyr	His	Lys	Lys	Ser	Gly	Thr	Thr	Ser	Thr	Phe	
	105					110					115					120	
60	GAG	TCT	GCA	GCC	TTC	CCT	GGT	TGG	TTC	ATC	GCT	GTC	TGC	TCT	AAA	GGG	497
	Glu	Ser	Ala	Ala	Phe	Pro	Gly	Trp	Phe	Ile	Ala	Val	Cys	Ser	Lys	Gly	
					125					130					135		
65	AGC	TGC	CCA	CTC	ATT	CTG	ACC	CAA	GAA	CTG	GGG	GAA	ATC	TTC	ATC	ACT	545
	Ser	Cys	Pro	Leu	Ile	Leu	Thr	Gln	Glu	Leu	Gly	Glu	Ile	Phe	Ile	Thr	
				140					145					150			

GAC TTC GAG ATG ATT GTG GTA CAT TAAGGTTTTT AGACACATTG CTCTGTGGCA 599  
Asp Phe Glu Met Ile Val Val His  
155 160

5

CTCTCTCAAG ATTTCTTGGG TTCTAACAAG AAGCAATCAA AGACACCCCT AACAAAATGG 659

AAGACTGAAA AGAAAAGCTGA GCCCTCCCTG GGCTGTTTTT CCTTGGTGGT GAATCAGATG 719

10 CAGAACATCT TACCATGTTT TCATCCAAAG CATTTACTGT TGGTTTTTAC AAGGAGTGAA 779

TTTTTTAAAA TAAAATCATT TATCTCATAA 809

15 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25

Met Asn Lys Glu Lys Glu Leu Arg Ala Ala Ser Pro Ser Leu Arg His  
1 5 10 15

30

Val Gln Asp Leu Ser Ser Arg Val Trp Ile Leu Gln Asn Asn Ile Leu  
20 25 30

Thr Ala Val Pro Arg Lys Glu Gln Thr Val Pro Val Thr Ile Thr Leu  
35 40 45

35 Leu Pro Cys Gln Tyr Leu Asp Thr Leu Glu Thr Asn Arg Gly Asp Pro  
50 55 60

Thr Tyr Met Gly Val Gln Arg Pro Met Ser Cys Leu Phe Cys Thr Lys  
65 70 75 80

40

Asp Gly Glu Gln Pro Val Leu Gln Leu Gly Glu Gly Asn Ile Met Glu  
85 90 95

45 Met Tyr Asn Lys Lys Glu Pro Val Lys Ala Ser Leu Phe Tyr His Lys  
100 105 110

Lys Ser Gly Thr Thr Ser Thr Phe Glu Ser Ala Ala Phe Pro Gly Trp  
115 120 125

50 Phe Ile Ala Val Cys Ser Lys Gly Ser Cys Pro Leu Ile Leu Thr Gln  
130 135 140

55 Glu Leu Gly Glu Ile Phe Ile Thr Asp Phe Glu Met Ile Val Val His  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 177 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu  
1 5 10 15  
Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser  
20 25 30  
Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe  
35 40 45  
Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn  
50 55 60  
Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala  
65 70 75 80  
Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys  
85 90 95  
Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp  
100 105 110  
Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser  
115 120 125  
Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp  
130 135 140  
Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn  
145 150 155 160  
Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp  
165 170 175  
45 Glu

(2) INFORMATION FOR SEQ ID NO:8:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met  
1 5 10 15

Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn  
20 25 30

10 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile  
35 40 45

Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro  
50 55 60

15 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg  
65 70 75 80

Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met  
85 90 95

20 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys  
100 105 110

Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile  
115 120 125

25 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly  
130 135 140

30 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe  
145 150 155 160

Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys  
165 170 175

35 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu  
180 185 190

40 Asp

## (2) INFORMATION FOR SEQ ID NO:9:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met  
1 5 10 15

60 Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu



	20	25	30
	Glu Ser Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg		
	35	40	45
5	Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe		
	50	55	60
10	Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg		
	65	70	75
	Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val		
	85	90	95
15	Thr Leu Ser Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn		
	100	105	110
	Lys Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp		
	115	120	125
20	Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn		
	130	135	140
25	Lys Met Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys		
	145	150	155
	Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu		
	165	170	175
30	Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser		
	180	185	190

## (2) INFORMATION FOR SEQ ID NO:10:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: peptide

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

50	Met Ala Glu Val Pro Lys Leu Ala Ser Glu Met Met Ala Tyr Tyr Ser	
	1	5
	Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln Met	
	20	25
55	Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile	
	35	40
	Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala	
60	50	55
		60

Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro  
 65 70 75 80  
 5 Cys Pro Gln Thr Phe Gln Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe  
 85 90 95  
 Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala  
 100 105 110  
 10 Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp  
 115 120 125  
 Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala  
 130 135 140  
 15 Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met  
 145 150 155 160  
 Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu  
 165 170 175  
 Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp  
 180 185 190  
 25 Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys  
 195 200 205  
 Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn  
 210 215 220  
 30 Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr  
 225 230 235 240  
 Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly  
 245 250 255  
 35 Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser  
 260 265

40 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids  
 (B) TYPE: amino acid  
 45 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

55 Met Ala Lys Val Pro Asp Met Phe Glu Asp Leu Lys Asn Cys Tyr Ser  
 1 5 10 15  
 Glu Asn Glu Glu Asp Ser Ser Ser Ile Asp His Leu Ser Leu Asn Gln  
 20 25 30  
 60

Lys Ser Phe Tyr His Val Ser Tyr Gly Pro Leu His Glu Gly Cys Met  
 35 40 45  
 5 Asp Gln Ser Val Ser Leu Ser Ile Ser Glu Thr Ser Lys Thr Ser Lys  
 50 55 60  
 Leu Thr Phe Lys Glu Ser Met Val Val Val Ala Thr Asn Gly Lys Val  
 65 70 75 80  
 10 Leu Lys Lys Arg Arg Leu Ser Leu Ser Gln Ser Ile Thr Asp Asp Asp  
 85 90 95  
 Leu Glu Ala Ile Ala Asn Asp Ser Glu Glu Glu Ile Ile Lys Pro Arg  
 100 105 110  
 15 Ser Ala Pro Phe Ser Phe Leu Ser Asn Val Lys Tyr Asn Phe Met Arg  
 115 120 125  
 20 Ile Ile Lys Tyr Glu Phe Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile  
 130 135 140  
 Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Ala Leu His Asn Leu  
 145 150 155 160  
 25 Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp  
 165 170 175  
 Asp Ala Lys Ile Thr Val Ile Leu Arg Ile Ser Lys Thr Gln Leu Tyr  
 180 185 190  
 30 Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro  
 195 200 205  
 35 Glu Ile Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe  
 210 215 220  
 Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro  
 225 230 235 240  
 40 Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala Gly  
 245 250 255  
 Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln Ala  
 260 265 270

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..504

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5      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 144
          (D) OTHER INFORMATION: /note= "nucleotide 144 designated
      G, may be G or T"

      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 451
          (D) OTHER INFORMATION: /note= "nucleotide 451 designated
      C, may be C or T"

      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 469
          (D) OTHER INFORMATION: /note= "nucleotide 469 designated
      C, may be A, C, G, or T"

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

      ATG AGA GGC ACT CCA GGA GAC GCT GAT GGT GGA GGA AGG GCC GTC TAT      48
      Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
          1             5             10             15

      CAA TCA ATG TGT AAA CCT ATT ACT GGG ACT ATT AAT GAT TTG AAT CAG      96
      Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
          20             25             30

      CAA GTG TGG ACC CTT CAG GGT CAG AAC CTT GTG GCA GTT CCA CGA AGG      144
      Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Arg
          35             40             45

      ACC AGT GTG ACC CCA GTC ACT GTT GCT GTT ATC ACA TGC AAG TAT CCA      192
      Thr Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
          50             55             60

      GAG GCT CTT GAG CAA GGC AGA GGG GAT CCC ATT TAT TTG GGA ATC CAG      240
      Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
          65             70             75             80

      AAT CCA GAA ATG TGT TTG TAT TGT GAG AAG GTT GGA GAA CAG CCC ACA      288
      Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
          85             90             95

      TTG CAG CTA AAA GAG CAG AAG ATC ATG GAT CTG TAT GGC CAA CCC GAG      336
      Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
          100            105            110

      CCC GTG AAA CCC TTC CTT TTC TAC CGT GCC AAG ACT GGT AGG ACC TCC      384
      Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
          115            120            125

      ACC CTT GAG TCT GTG GCC TTC CCG GAC TGG TTC ATT GCC TCC TCC AAG      432
      Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
          130            135            140

      GGA GAC CAG CCC ATC ATT CTG ACT TCA GAA CTT TGG CAG TCA TAC AAC      480
      Gly Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Trp Gln Ser Tyr Asn
          145            150            155            160

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ACT GCC TTT GAA TTA AAT ATT AAT G  
Thr Ala Phe Glu Leu Asn Ile Asn  
165

505

5

## (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 168 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr  
1 5 10 15  
20 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln  
20 25 30  
25 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Arg  
35 40 45  
Thr Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro  
50 55 60  
30 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln  
65 70 75 80  
Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr  
85 90 95  
35 Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu  
100 105 110  
40 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser  
115 120 125  
Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys  
130 135 140  
45 Gly Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Trp Gln Ser Tyr Asn  
145 150 155 160  
Thr Ala Phe Glu Leu Asn Ile Asn  
165

50

## (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 1195 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 67..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10	CCACGATTCA	GTCCCCTGGA	CTGTAGATAA	AGACCCTTTC	TTGCCAGGTG	CTGAGACAAC	60
	CACACT	ATG AGA GGC ACT CCA GGA GAC GCT GAT GGT GGA GGA AGG GCC	108				
	Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala						
	1	5	10				
15	GTC TAT CAA TCA ATG TGT AAA CCT ATT ACT GGG ACT ATT AAT GAT TTG	156					
	Val Tyr Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu						
	15	20	25	30			
20	AAT CAG CAA GTG TGG ACC CTT CAG GGT CAG AAC CTT GTG GCA GTT CCA	204					
	Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro						
	35	40	45				
25	CGA AGT GAC AGT GTG ACC CCA GTC ACT GTT GCT GTT ATC ACA TGC AAG	252					
	Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys						
	50	55	60				
30	TAT CCA GAG GCT CTT GAG CAA GGC AGA GGG GAT CCC ATT TAT TTG GGA	300					
	Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly						
	65	70	75				
35	ATC CAG AAT CCA GAA ATG TGT TTG TAT TGT GAG AAG GTT GGA GAA CAG	348					
	Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln						
	80	85	90				
40	CCC ACA TTG CAG CTA AAA GAG CAG AAG ATC ATG GAT CTG TAT GGC CAA	396					
	Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln						
	95	100	105	110			
45	CCC GAG CCC GTG AAA CCC TTC CTT TTC TAC CGT GCC AAG ACT GGT AGG	444					
	Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg						
	115	120	125				
50	ACC TCC ACC CTT GAG TCT GTG GCC TTC CCG GAC TGG TTC ATT GCC TCC	492					
	Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser						
	130	135	140				
55	TCC AAG AGA GAC CAG CCC ATC ATT CTG ACT TCA GAA CTT GGG AAG TCA	540					
	Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser						
	145	150	155				
60	TAC AAC ACT GCC TTT GAA TTA AAT ATA AAT GAC TGA ACT CAGC CTAGAGGTGG	593					
	Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp						
	160	165					
65	CAGCTTGGTC TTTGTCTTAA AGTTTCTGGT TCCCAATGTG TTTTCGTCTA CATTTTCTTA	653					
	GTGTCATTTT CACGCTGGTG CTGAGACAGG GGCAAGGCTG CTGTTATCAT CTCATTTTAT	713					
	AATGAAGAAG AAGCAATTAC TTCATAGCAA CTGAAGAACA GGATGTGGCC TCAGAAGCAG	773					

	GAGAGCTGGG	TGGTATAAGG	CTGTCCTCTC	AAGCTGGTGC	TGTGTAGGCC	ACAAGGCATC	833
	TGCATGAGTG	ACTTTAAGAC	TCAAAGACCA	AACACTGAGC	TTTCTTCTAG	GGGTGGGTAT	893
5	GAAGATGCTT	CAGAGCTCAT	GCGCGTTACC	CACGATGGCA	TGACTAGCAC	AGAGCTGATC	953
	TCTGTTTCTG	TTTTGCTTTA	TTCCCTCTTG	GGATGATATC	ATCCAGTCTT	TATATGTTGC	1013
	CAATATACCT	CATTGTGTGT	AATAGAACCT	TCTTAGCATT	AAGACCTTGT	AAACAAAAAT	1073
10	AATTCCTGTG	TTAAGTTAAA	TCATTTTTGT	CCTAATTGTA	ATGTGTAATC	TTAAAGTTAA	1133
	ATAAACTTTG	TGTATTTATA	TAATAATAAA	GCTAAAACTG	ATATAAAAAA	AAAAAAAAAA	1193
15	AA						1195

(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30 Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr  
 1 5 10 15

Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln  
 20 25 30

35 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser  
 35 40 45

Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro  
 50 55 60

40 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln  
 65 70 75 80

45 Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr  
 85 90 95

Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu  
 100 105 110

50 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser  
 115 120 125

Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys  
 130 135 140

55 Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn  
 145 150 155 160

Thr Ala Phe Glu Leu Asn Ile Asn Asp  
 165